

Genome Announcement

The Complete Genome Sequence of *Campylobacter jejuni* Strain 81116 (NCTC11828)[▽]

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***Campylobacter jejuni* is a major human enteric pathogen that displays genetic variability via genomic reorganization and phase variation. This variability can adversely affect the outcomes and reproducibility of experiments. *C. jejuni* strain 81116 (NCTC11828) has been suggested to be a genetically stable strain (G. Manning, B. Duim, T. Wassenaar, J. A. Wagenaar, A. Ridley, and D. G. Newell, Appl. Environ. Microbiol. 67:1185–1189, 2001), is amenable to genetic manipulation, and is infective for chickens. Here we report the finished annotated genome sequence of *C. jejuni* strain 81116.**

The complete genome sequence of *Campylobacter jejuni* strain 81116 (NCTC11828) (4) was determined using a combination of shotgun sequencing (GATC Biotech, Germany) and 454 pyrosequencing technology (454 Life Sciences, Branford, CT). The *C. jejuni* 81116 isolate used in this study was first confirmed to be infective for chickens by experimental infection, and the strain was minimally passaged afterwards before being used for the determination of the genome sequence. Draft assemblies were based on 419,928 total reads. All libraries provided 30-fold coverage of the genome. The initial assembly of the 454 pyrosequencing data into 45 contigs was provided by 454 Life Sciences (Branford, CT), whereas the contig assembly step of the shotgun sequencing was performed using SeqMan (DNASTar Inc., Madison, WI) with the *C. jejuni* NCTC11168 genome sequence (6) as a scaffold. Gaps between contigs were closed by PCR amplification followed by DNA sequencing (John Innes Genome Laboratory, Norwich, United Kingdom).

The *C. jejuni* 81116 (NCTC11828) genome was found to be 1,628,115 bp long and contains 1,626 putative open reading frames. The average G+C content is 30.54%, and there are 44 tRNAs and 3 rRNA operons. *C. jejuni* strain 81116 (NCTC11828) does not contain plasmids (4). *C. jejuni* strain 81116 (NCTC11828) contains 17 homopolymeric G tracts (defined as tracts of ≥ 7 consecutive G residues), fewer than the

other complete *C. jejuni* genome sequences described to date (29 in NCTC11168, 25 in RM1221, and 19 in 81-176) (3, 5, 6). A high degree of variation in these G tracts was noticed already in the shotgun phase of the sequencing and was confirmed using PCR and G tract fingerprinting. A unique feature of the *C. jejuni* 81116 (NCTC11828) genome sequence is the duplication of a 6.5-kb region that is not duplicated in the genome sequences of *C. jejuni* strains NCTC11168 (2, 6), 81-176 (3), RM1221 (5), and CG8486 (7). Furthermore, some genes described as pseudogenes in other strains are complete open reading frames in *C. jejuni* 81116 (e.g., Cj0444 and C8J_0419, respectively), whereas other pseudogenes are still present (e.g., Cj0046 and C8J_0049, respectively). Finally, the *C. jejuni* 81116 (NCTC11828) genome contains only a single gene encoding TonB, compared to two or three genes in other *C. jejuni* strains, and lacks the CfrA and Cj0178 outer membrane receptors for iron uptake (1).

The genome sequence of *C. jejuni* is subject to evolutionary change, which can be mediated via mobile genetic elements, the uptake of DNA via natural transformation, and changes in hypervariable sequences like the G tracts described above. Changes in hypervariable G tract lengths present a challenge to researchers interested in the biology of *C. jejuni*, and these regions should be routinely monitored during experiments. *C. jejuni* strain 81116 (NCTC11828) is genetically amenable, is infective for chickens, and has been reported to be genetically stable (4). Since *C. jejuni* 81116 (NCTC11828) has fewer hypervariable G tracts than other strains sequenced so far (3, 5–7), it may prove to be a more stable and reliable strain suitable for in vitro and in vivo experiments.

Nucleotide sequence accession number. The complete sequence of the *C. jejuni* strain 81116 (NCTC11828) genome can be accessed under the GenBank accession number CP000814.

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